PTO/SB/08B (10-01)

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Substitute for form 1449B/PTO

NFORMATION DISCLOSURE STATEMENT BY APPLICANT

(use as many sheets as necessary)

Sheet οf

Complete if Known				
Application Number	10/160,293			
Filing Date	June 4, 2002			
First Named Inventor	Erika Lindquist et al.			
Group Art Unit	1645			
Examiner Name	TBA			
Attorney Docket Number	CL001241			

OTHER REIGHT AND RATENT LITERATURE DOCUMENTS				
OTHER PRIOR ART – NON PATENT LITERATURE DOCUMENTS				
Examiner Initials	Cite No. ¹	Include name of the author (in CAPITAL LETTERS), title of the article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc.), date, page(s), volume-issue number(s), publisher_city and/or country where published.	T ²	
· · · · · · · · · · · · · · · · · · ·		Results of BLAST search of SEQ ID NO:2 against Derwent (FastAlert and GeneSeqP) and NCBI (pataa) protein patent databases on October 9, 2003.		
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Burden Hour Statement: This form is estimated to take 2.0 hours to complete. Time will vary depending upon the needs of the individual case. Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, Washington, DC 20231. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. SEND TO: Assistant Commissioner for Patents, Washington, DC 20231.

^{*}EXAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

¹ Applicant's unique citation designation number (optional). ² Applicant is to place a check mark here if English language Translation is attached.

7-2000

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Erika Lindquist et al.

Art Unit: 1645

Serial No.: 10/160,293

Examiner: TBA

Filed: June 4, 2002

Atty. Docket: CL001241

For: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE

PROTEINS, AND USES THEREOF

Statement Regarding Duty to Disclose Information Material To Patentability Under 37 CFR 1.56 (a) and (b)

Assistant Commissioner for Patents Washington, D.C. 20231

Sir:

Applicants hereby notify the US Patent and Trademark Office of the documents listed on the attached PTO Form SB/08A, which may be deemed relevant to the patentability of the claims of the above application. One copy of each of the listed documents is submitted herewith. The submission of the listed documents is not intended as an admission that any such document constitutes prior art against the claims of the present application.

No fee is due for this submission. However, the Patent and Trademark Office is authorized to charge any necessary fees related to the processing of this application to Deposit Account No. 50-0970.

Respectfully submitted,

CELERA GENOMICS

Date: October 31, 2003

Celera Genomics 45 West Gude Drive, C2-4#21 Rockville, MD 20850

Tel: 240-453-3812 Fax: 240-453-3084

Patent Screen Results

Your Fasta Input (protein sequence):

>CL001241, SEQ ID NO:2, October 9, 2003

- 1 MGFLGTGTWI LVLVLPIQAF PKPGGSQDKS LHNRELSAER PLNEQIAEAE
- 51 EDKIKKTYPP DDPDGLHQLD GTPLTAEDIV HKIAARIYEE NDRAVFDKIV
- 101 SKLLNLGLIT ESQAHTLEDE VAEVLQKLIS KEANNYEEDP NKPTSWTENQ
- 151 AGKIPEKVTP MAAIQDGLAK GENDETVSNT LTLTNGLERR TKTYSEDNFR
- 201 DFQYFPNFYA LLKSIDSEKE AKEKETLITI MKTLIDFVKM MVKYGTISPE
- 251 EGVSYLENLD EMIALQTKNK LEKNATDNIS KLFPAPSEKS HEETDSTKEE
- 301 AAKMEKEYGS LKDSTKDDNS NPGGKTDEPK GKTEAYLEAI RKNIEWLKKH
- 351 DKKGNKEDYD LSKMRDFINK QADAYVEKGI LDKEEAEAIK RIYSSL

FastAlertP Blast Report:

BLASTP 2.0.14 [Jun-29-2000]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= CL001241, SEQ ID NO:2, October 9, 2003 (396 letters)

Database: /work/eda/blast/public/FastAlert_P.fasta 427,960 sequences; 98,452,735 total letters

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Score
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Sequences producing significant alignments:
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Sbjct: 133 DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE 192
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Ident. Query: Sbjct: Query: Sbjct: Query:	= 6 itie: 61 133 121 193	Length = 468 668 bits (1706), Expect = 0.0 5 = 333/336 (99%), Positives = 334/336 (99%) DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT	192 180 252 240
Ident: Query: Sbjct: Query: Sbjct: Query:	= 6 ities 61 133 121 193 181 253	Length = 468 668 bits (1706), Expect = 0.0 5 = 333/336 (99%), Positives = 334/336 (99%) DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPAPSEKSHEETDSTKEE	192 180 252 240 312
Ident: Query: Sbjct: Query: Sbjct: Query: Sbjct: Query:	= 6 itie: 61 133 121 193 181 253 241	Length = 468 668 bits (1706), Expect = 0.0 5 = 333/336 (99%), Positives = 334/336 (99%) DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM	192 180 252 240 312 300
Ident: Query: Sbjct: Query: Sbjct: Query: Sbjct: Query:	= 6 ities 61 133 121 193 181 253 241 313	Length = 468 668 bits (1706), Expect = 0.0 5 = 333/336 (99%), Positives = 334/336 (99%) DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPAPSEKSHEETDSTKEE MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPAPSEKSHEETDSTKEE MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPAPSEKSHEETDSTKEE	192 180 252 240 312 300 372
Ident: Query: Sbjct: Query: Sbjct: Query: Sbjct: Query:	= 6 ities 61 133 121 193 181 253 241 313 301	Length = 468 668 bits (1706), Expect = 0.0 5 = 333/336 (99%), Positives = 334/336 (99%) DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM LTLTNGLERRTKTYSEDNF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPAPSEKSHEETDSTKEE MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPAPSEKSHEETDSTKEE	192 180 252 240 312 300 372 360
Ident: Query: Sbjct: Query: Sbjct: Query: Sbjct: Query: Sbjct: Sbjct:	= 6 ities 61 133 121 193 181 253 241 313 301 373	Length = 468 668 bits (1706), Expect = 0.0 5 = 333/336 (99%), Positives = 334/336 (99%) DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE DDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDE VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT VAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNT LTLTNGLERRTKTYSEDNFRDFQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM LTLTNGLERRTKTYSEDNFF + QYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM LTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKM MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPAPSEKSHEETDSTKEE MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPAPSEKSHEETDSTKEE MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPAPSEKSHEETDSTKEE MVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPAPSEKSHEETDSTKEE AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD	192 180 252 240 312 300 372 360

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Query: 301 AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYD 360